

SEQUENCE LISTING

SEQ. ID. No. 1

3bf4 3000 bp

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SEQ. ID. No. 2

SEQ. ID. No.

1011 25 bp
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SEQ. ID. No. 3

cc49 1507 bp

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 SEQ. ID. No. 4

cc43 2605 bp

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SEQ. ID. No. 5

41.1 1288 bp

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SEQ. ID. No. 6

GCAP 2820 bp

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1b4 1205 bp

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SEO, ID. No. 8

20sa7 456 hp

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SEQ. ID. No. 9

Genomic Sequence Encoding ZABC1

Genomic sequence, Encoding ZABC1
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85 TCCCCATCTCAGACAACGCTGCCAGGAATGGGTTTGGAGAGGCCAGACTCAAGTCCAGGCTTCTGACCTCGCCGCCCCCTCTG
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90 CCTGTTCTGAAAATATATATTTAAACGTGATCTGTTCTGTCACAAAACACACTTTAAAAAAATA
ACTTGTGCTCATCCAGGAAAATGCACTGCTTAACTGGGCTTCTGTCAGTGTGAGGATGGCTTCCGAGGAAATCC
95 GAGGCTTGGTGTCTGAGTGTGAGGGCTTCTGTCAGTGTGAGGGAGCTGTTCTGTCAGTGTGAGGATGGCTTCCGAGGAAATCC
CAGCATGGTACAGTGCACAGGACAGCCCCATCATCAAAGAATTCTGTCAGTGTGAGGATGGCTTCCGAGGAAATCC
AGAGACCTAGCCTCACTTAAAGTTTCTGGCTCTGATCTGTCAGTGTGAGGATGGCTTCCGAGGAAATCC
100 GGTACTGGGAGTGAACACTAGGCCAGGAATTATTTGGGAGGCCGGTCTGTCAGTGTGAGGATGGCTTCCGAGGAAATCC
CTGTCTGCCAGACTATCCATTAGGTACCTCAGGAACCCAAATGATGTCATTTAAACAGGAAATCC
GCACACTGAAGACATTAAAGAAGGCTCATTGTCAGCAGAACCTGTCAGGAACTGTCAGTGTGAGGATGGCTTCC
105 GAAGGTGATCACTGAAGGAGCTGTCACATAATATTCTGAGGCCCTGGCTTCTGTCAGTGTGAGGATGGCTTCC
CTGTCAGTGTGAGGATGGCTTCCGAGGAAACAGGAAACCCAGCACTTACGACTACAAATCTAATGCTTAA
GGATCTGGCTTAAACAGTTGAAAGACCTGTAGGGCAGGCCGTAATTGACAAGCGAATGATGGGAAACATGA
110 ATCGGTCTAGGGAGCATCTGTCACAGTGGCTTAAACAGTGGCTTGGTAAACAGTGGCTTCCCTCTCAGTGTCACTGGATT
GTGTGCTGAAATTCTGGAAAAGCTGGGTATGAGACCCACGATGAAATTGCCCACACGATTGATTGAGCTCTC
115 CTTCACCTGCTTCAAGCCAGTGCCTGAGCTTCTTCTGATCATGTCAGTGTGAGGACTGTCAGTGTGATATCA
AATCTTAAAGTGTGAGTTCTGGACACAGAACCCAGCACTTACGACTACAAATCTAATGCTTAA
TGGCATCATAAAAGAGGCTTAAACACAGACTCCAGTACGTTGAGGCTTCTGTCAGTGTGAGGACTGTCAG
120 GGGCCCTGTGAGGATGCCCTGGCTTCTGAAAGAATGAAAAGGGCAGTACCGGGTAGGTGGTGGAAAACATGG
CTAGATCATCAGGCCAGGACAGAACGTCCTGGCTGTTGGAGCACCACGCTGGCTTGGAGTTCTGGTCT
ACTGGCTTGTGAGTTGACCAATTATGAGTTGCTTAACTTCTTGTACTATTCTCTGTCACAGTGTGAGGTTCA
125 TTGACCCCTGCTTCCACCTCCAAAGGACAATTCAACGCCATTGTAAGGATCACAGTCTTAAATA
130

SEQ. ID. No. 10

ZABC1 Open reading frame

65 ATGCAATCGAAAGTGACAGGAAACATGCCAACTCAATCCCTCTTAATGTACATGGATGGGCCAGAAGTATTGGCA
GCTCTTGGCAGTCCGATGGAGATGGAGGATGCCCTGTCATGAAAGGGACCGCTGTTGTCATTCCGAGCTAC
ACAAGAAAAAAATGTCATCCAAATCGAGGGGTATATGCCCTGATTGCACTGTCAGCCAGACCTTCACACAT
TCAGAAGACCTTAATAAACATGCTTAATGCAACACCGGCCTACCCCTGTCAGACCAGCAGTTCTGGGTTGAAG
CAGAGTATCTCAGTCCGCTTGTATAAAAGTCAGTGGCAACAGAACCTCCCAGGAAAAGAATTGCAAGGAAAATGA
ATTAGCTGTGGATGTGGGAGACATTAGTCGCTTTGATGTTGAGATCCACATGAGAACACACAAAGAT
70 TCTTCACTTACGGGTGTAACATGTGCGGAAGAGMTTSRRSSAGCCTTGGTTCTTAAAAATCACATGCGGACAC
ATAATGGCAAATCGGGGCCAGAAGCAAACATGCGCAAGGCTTGGAGAGTAGTCAGCAACGATCAACGAGGTCGT
CCAGGTGCACGCGGGCAGAGCATCTCCTCTTACAAAATCTGCATGGTTGTGGCTTCCATTTCAAAATAAAA

5 GAAAGTCTAATTGAGCACCGCAAGGTGCACACCAAAAAACTGCTTCGGTACCAGCAGCGCGCAGACAGACTCTC
 CACAAGGAGGAATGCCGTCTCGAGGGAGGACTTCCTGCAGTTGCAACTTGAGACCAAAATCTCACCCCTGAAAC
 GGGGAAGAAGCCTGTCAGATGCATCCCTCAGCTCGATCCGTTACCCACCTTCCAGGCTTGGCAGCTGGCTACCAA
 GGAAAAGTTGCCATTGCCAAGAAGTGAAGGAATCGGGCAAGAAGGGAGCACCACAGCAGCTGGCTACCAA
 AGAAGGAGCTTGGAGAACAAATAAGGGCAGTTGTCAGGCTCTCGCAAGAGAGAAAGAGAAAGTGCACACACTCCA
 CGCGAAGGCCCTCGTGACGGATCCCAAGTACCTCCAGTGCAGGAGAAAGCCACTCACTGCTCCGAGTGC
 GCAAAGCTTCAAGAACCTACCAACAGCTGGTCTGCACCTCCAGGCTCCACAAGAAGGAGCGGAGGGCCGCG
 AGTCGCCACCATGTCGTGACGGATCTGAGGATGGCTTCCGAAGGAATCCATCTGGAT
 10 TGGAGCGTGGATCGAGGGAGGGAGGTGTTCTGAAGACGGATCTGAGGATGGCTTCCGAAGGAATCCATCTGGAT
 AAAATGATGATGGAGGAAAAAAACATCTTACATCTTCAAGAGAGTGTAGTTATTGTGAAAGTGTGAAAGTTTCCGTT
 CAAATTATTACCTCAATATTCACTCAGAACGACATAGGTGAAAACCATACAAATGTGAATTGTGAAATATGC
 TGCAAGCCCAGAACAGACATCTGAGGTACTTGGAGAGACATCACAGGAAAAACAAACCGATGTTGCTGCTGAA
 GTCAAGAACGATGGTAAAATCAGGACACTGAAGATGCACTTAAACCCTGACAGTGCAGAAGGAGATGCTTCTGTTT
 15 AAAGATTTTGATGGTGCAGGAAAGATGTTACAGGAGCTGCAACAGCAGCTTAAAGGAGATGCTTCCATAAAATGAGCTGAT
 TCAGAATGTTCTGGCAGCGCTGTCCTCACCAGCACAAAGAATACTCAGGATTTCCATAAAAGAGATCAGCAGTGT
 GACAGTGCCTGATAAAACTGAATAAAACCCCTACCCCTGCTTACCTGGACCTGTTAAAAGAGATCAGCAGTGT
 CTCAGGCAAATAACCTCATCTGAGAACCAAGGGCGATGTTACTCCTCCGGATGGCAGTACCCATAACCT
 TGAAAGTTAGCCCCAAAGAGAACAGAACAGGAGACCCAGCTGACTGCAGATACAGGCCAAGTGTGATTGTCAGGAA
 20 AAACCTTAAATTATCCGTGGGGCTTCAACAATTGCCCAGCAATTCTTGAAGTAAAGTTGAGTAAAGTTGATTCCAAGTA
 TCACCTGTCATTGTCACCTCAAGACATTATCAGAACAGTTTAATGTCAGCACCAGAGACTGGAGCATAAAATA
 CAATCTGACGTTCAAAACTCTGCAAGAACACTCTGCTTAAACAGCCAACTGCTGCTTCCGGCAGTGGCAGTGGATTGTCAGGAA
 CTGGAAAAGATGTGCTCCCTCTCTAGTTCTGAAACCCAAGGCCAAGTCTGCTTCCGGCAGTGGCAGTGGATTGTCAGGAA
 CCCTGCCATCTGCCAAGGGAGCAGAGCCCTCTGGGCCAGGCAAGGCCCTCTGACTCAGGGATAGACTCTAG
 CACTTAGCCCCAAGTAACCTGAAGTCCCACAGACCACAGCAGAACATGTGGGGTCCAAGGGGCCACCAGGCAA
 25 CAGCAATCTGAGATGTTCTAAACCAAGTGTTCCTGCACCGATAAGACAAAAAGACCCGAGACAAATTGAA
 AACCTTCCAGTAGCTCTCAGCCCACCTCGCAGCAGTAACATCAATGGTCCATGACTACCCGCAA
 GAACGACAGCCCGTGGCACCTCCGGAAAGAGACTATTCTGTAATCGGAGTGCCAGCAACTACTGCAGCAGAATT
 GGTGAGCCCCCTCCAAAAGACTGAAGTCCAGCTGGTGGCTGCCCTGACCTGACCAGCCGGGCCAATTACAGAA
 30 GAGGCTATGACCTTCCAAGTACCATATGGTCAGGGCATCACATCACTGTTACCCGAGGACTGTGTATCCGTC
 GCAGGGCCTGCCCTCCAAAAGGTTCTGAGCTCCAGCAGGTCGATTCTCAAATGTGCTGACTGTTGAGAAG
 CCCTATGGTGGCTCCGGGCCACTTACACTTGTGCTGCTGTTAGTCCAGCATCCAGCTCGACGTTAGAAGGTC
 TTGGTGGATGTCAGTCTACTCCCCATGAAATTAAATTACTCATCTTGAAGAAGCAGAATGGTAAAGTC
 TGAAATAAGCTGTGATTGACTGTACATAAAACATATGAGGAATCTGCAAGGAACACTACAGTTGTAA

35 SEQ. ID. No. 11

ZABC1 Protein

MQSKVTGNMPTQSLLMYMDGPEVIGSSLGSPMEMEDALSMKGTAVVPFRATQEKNVIQIEGYMPLDCMFCSQTFH
 SEDLNKHVLQMHRPTLCEPAVLRVEAEYLSPLDKSQVRTEPPKEKNCKENEFSEVCQQTFRVAFDVEIHMRTHKD
 SFTYGCNCGRXXXXPWFLKNHMRTNGKSGARSKLQQGLESSPATINEVVQVHAAESEISSPVKICMVCGLFPNK
 40 ESLIEHRKVHTKKTAGTSSAQTDSPQGGMPSSREDFLQLFNLRPKSHPETGKPKVRCIPQLDPFTTFQAWQLATK
 GKVAICQEVKESQEGSTNDSSSEKELGETNKGSCAGLSQEKEKCKHSHGEAPSVDADPKLPSSEKPKTHCSEC
 GKAFRTYVHLHSRVRHKDRAGAESPMSVDSGRQPGTCSPDLAALPDLENGAVDRGEGGSEDGSEDGLPEGIHL
 KNDDGGKIKHLTSRECSYCGKFRSNNYLNHLRHTGEKPKCEYAAQKTSRHYLERHKEKQTDVAAE
 VKNDGKNQDTEALLTADSAQTKNLKRFFDGAKDVTGSPPAKQLKEMPSVQNVLGSALSPAHKDQDFHKNAAD
 45 DSADKVKNPPTPAYLDLLKKRSAVETQANNLICRTKADVTPPDGSTTHNLEVPSPKEQKTEAADCYRPSVDCE
 KPLNLSVGAHNCPAISLSKSLIPSITCPCTFKTFYYPEVLMMHQRLEHKYNPDVHKNCRNKSLRSRTGCPP
 LGKDVPPLSSPCPKPKSAFPAQSKSLPSAKGKQSPPGPGKAPLTSGIDSSTLAPSNLKSHRPQNVGVQGAATRQ
 QQSEMFPKTSVSPAPDKTRPETKLKPLPVAPSQPTLGSNNINGSIDYPAKNDSPWAPPGRDYFCNRSASNTAAEF
 50 GEPLPKRLKSSVALDVQPGANYRRGYDLPKYHMVRGITSLLPQDCVYPSQALPPKPRFLSSVEDSPNVLTVQK
 PYGGSGPLYTCVPAGSPASSSTLEGGLGCQCLLPMKLNFTSSFEKRMVKATEISCDCTVHKTYEESARNTTVV

SEQ. ID. NO. 12

1b1

55 GGAAACAGCTATGACCATGATTACGCCAAGCTGAAATTAAACCTCACTAAAGGGAACAAAAGCTGGAGCTCCACC
 GCGGTGGCCGCCGCTCTAGAAACTAGTGGATCCCCGGCTGAGGAATTCCGCACGAGGCTCCACCCGACAGCCAG
 CACTGGGAGCAGCACTGGAGACCCAGGACCCCTGTCAGGAGCAGCTCCGGTGACACGAGGGACTGAAGATA
 TCCCACAGGGCTCAGCAGGACAATGGTAACCAATGAGTTCCCAAAGAGTTGAAGACCAAGAGAAATGAC
 CAGAACAGCAGACTTACCAAGGACAACGCCGCTCTGAAACGGGTTCCAGTGTGGTGCACCCACACAGTTCA
 GCACCTAGAGGAAGTCGACTTGGGATAATGTCAGAACAGGATAATGTGGCCACTTCTCCCCGAGAACACGGAG
 60 ATAAGTGTGTTGGGATGCCAACGGAAAATCTGGGAAAGAGGGCCAAACCCGAGGCACCGACTGCTAAATCTC
 GTTTTTCTGATGCTCTCGGCCCTGACAGGAGCTTACAGGAGCTACGGAGACCAAGGCCAGATTCATCCCTGGATCAGT
 GAAGCTTGTGTCAGCTCAAATAAGCTCCAGCGAACAAAGACCCAGTGGAGACTTCCGGTGGCAGCT
 GGACCGGGGAGGACACAGATAAAACCCAGGGCACGCCGGCCAGACAAAGGTCTCTGCCCAGGGATC
 CCACGCTCTCCACCTGAGACAGGGGAGCAGGAGGAGAACCTCCCAAGGCCAAGGACTCCAGCTTTTGA
 65 CAAATTCTCAAGCTGGACAAGGGACAGGAAAGGTGCCAGGTACAGCCAAACAGGAAGCCAAGAGGGCAGAGCAT
 CAAGACAAGGTGGATGAGGTTCTGGCTTATCAGGGCAGTCCGATGATGTCCTGCAGGGAGGACATAGTTGACG
 GCAAGGAAAAGAAGGACAAGAACCTGGAACTGGCAGTGGATTGCTCTGCTGCCAGGGACCCAGAAGGACTGGAGACTGC
 AAAGGAGGATTCCCAGGCAGCAGCTATAGCAGAGAATAATAATTCACTAGTGTGTTAAACTCTGGTTCA
 70 CCTAACAAAGCTGAAACAAAAAGGACCCAGAAGACACGGGCTGAAAAGTCACCCACCACTCAGCTGACCTTA
 AGTCAGACAAAGCCAACCTTACATCCCAGGAGACCCAGGGCTGGCAAGAATTCCAAGGATGCAACCCATCGGG
 GCACACACAGTCGTGACAACCCCTGAACCTGCGAAGGAAGGCACCAAGGAGAAATCAGGACCCACCTCTGCT

CTGGGCAAACGTGGAAAAAGTCAGTTAAAGAGGACTCAGTCCCCACAGGTGGGAGGAATGTGGTGTG
AGTCACCAGTAGAGATTATAAGTCAGGAACTAGAATCAGCTTACAAACAGTGGACCTCAACGAAGGAGATGC
5 TGACCTGAACCCACAGAAGCGAAACTCAAAAGAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCTTCTCAGA
CAAATGTCAGTGAAGGGGATGGAGGGATCACCACACTCAGAAGAAATAATGGGAAAGACTCCAGCTGCCAACAT
CAGACTCCACAGAAAAGACTATCACACCGCCAGAGCCTGAACCAACAGGAGCACCACAGAAGGGTAAAGAGGGCTC
CTCGAAGGACAAGAACGAGTCAGCAGCCAGATGAACAAAGCAGAAAGCAGCAACAGCAGGAAAGGCCAAGAACCCAG
TGCACAGAGCAGGCCACGGTGGACAGCAACTCAGTCAGAATGGGACAGCTCAGGTTCTCCACCAGGGTCTGCCACCAAGATGT
10 AGCAGTCCCTGGGGCTTCTTAAAGGCCTGGGACCAAGCGGATGTTGATGCTAAGTCAAACAGACCCAGT
ATCCATCGGACCAGTTGGCAACCCAAGTAAACAAATCAGCACGGTTCCACCAGGGTCTGCCACCAAGATGT
GTTCTCTTACTCCATCTCTCCCCAACACGCTCCATGTATATATTCTCTGATGGCCAGCAAATGAAATTCTGC
CTAGAAATTAAAGCCCAGCTGTTGATATTGAGGTGTATTACGTCTCTGGTCCAGTCTTCTGGCAAATAA
15 CAGTAAAGATGGTTAGCAGTCACCTAGTGGTCAGAAGAGTCGATGATACCAAGCAGGAAGGGAGGGAAATA
GAGGAATGTGTTGGGTTAAGTGTGATGAAAATGGCAGTGGTGGCCGGCGTGGTGGCTCTGCCGTGAATCTCAGCA
CTTGAGGGAGGCCAGGCAGGTGGATCAGCTGGTGGAGGAGTCAGACTAGCCTGCCAACATCATGAAACCCCG
TCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCCAACGC
20 ACGAGAACCGCTTGTACCCAGGAGGTGGAGGTTGAGTGGCAAGTTGACCATTGCACTCCACCCCTGGCGAC
AGAGCAAGATTCTATCAAAAAAAAAGGCAGTGGCAAGTAAGTTAGAAGAGAAATGCTGCTAGAAGGAATTAAAG
CGTTGTAGTAAACCGGTGCTATCCTCTAAGCTTGAAGAAGGGAGACGAAAATCATTGTTAAATTCAATCTC
AAGGAGGGAGAACCCGGGCTGTGTTGGGTTCCAATTCTAGAACCGAATGTGTTGGGTATAGAAAAAGGAA
TGAATAAGCGTTTTTCAAAATAGGGTCTTGTAAAGTTATTGATGAGAGGGAAAAGATTGACTGGGGAGGGCTTA
25 AAATGATTGGAAAACAATTGCTTTGAGGCTAGTGACAACGGCAAAGATTACAACCTTAAAAAAAAGGGGG
AAACTCGAGACTAGTTCTCTCTCTCGTGGCGAATTGATATCAAGCTTATCGATACCGTCGACCTCGAGGGG
GGGCCGGTACCCAAATTGCCCTATA

25

SEQ. ID. NO. 13

Genomic Sequence from BAC clone 97

Filtered query sequence:

>query_seq

5 TGTGATATTGATTCATGCCCTTGCACCTGCCAACATCACACGCTG
CCATCCAGTCCACTCGATTTGGCAGTGCAGATGAAAAACTGGGAACCAT
TTGTGTTGAGTCCAGCAAGATGCCAGGACCTGCATTTAGAACGAAAGT
TCTTCATCATCCAATTCTCCCTGTATATGGGCTTACACNACTGCCGTT
AAGTCGTGTNAAGTCACCACTCAGGTACATAATGGAATAATTCTGCAAAG
10 GCAGGAGNCACCTTCTCCAGTGCTCAGACCATGAAAGTTTCTGATGT
CTTGGAACTTGTCTGCAAATAGCTCGAAGGAGACATGGCCTAAAGGCT
CGCCATCTGCGGTGATATTGNAACATGGTAGGGCTGACCGTGGCTGTGGC
CATGACTTTAGANTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
15 NNN
NNNNNNNNNNNNNNCCAAATGCGGGACAGAGAACATCNAAGAAACTGTATT
GGGAAAGGGTCTGAGTTATGCCAAAGTTCCAGATTGGTTCCATTG
AAACGTAGCTGTGAGATACCATCAGGTGTTATGTGAAGAAATGTCTGT
GTAGTCAAATATGTTGAGTGAAGTGAAGCCTGAGCTGAGCAAGACTTACT
GCAAGACTTCCATCTCTGTCCTTTATGCTAATGGTAACACAAAC
20 TCCAAAAGTGGGTGTACAGCATGAGGCATTAACAAAAATTATTGGACC
CCACACACNN
NN
NN

25

SEQ ID NO 14

533 | RATCYC

8 418 (115,5,1,1) 7 1,5,52,5 1,17

Score = 418 (115.5 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58

Identities = 96/112 (85%), Positives = 96/112

S = rat CYCLOPHILLIN; q = SEQ ID NO 13.

Query: 312 AAAAGTTCCAAAGACATCAGAAAAACTTCTATGGTCTGAGCACTGGAGAGAAAG 261

Shict: 124 **AAAGTCC**AAAAGACAGCAGA**AAA**CTTTGCTGCTGTCAGGAGCTGGGGAGG 125

Subject: 114 AACCTTCAGAACAGCAGAAAACTTCGGTGCTTGAGGCACTGGGGAGAAAG 175

Score = 236 (65.2 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 52/58 (89%), Positives = 52/58 (89%), Strand = Xmax / D1

45 **INCORRECTS = 52/58 (89%), POSITIVES = 52/58 (89%), STRAND = Minus / Plus**

Query: 117 TGCTGGACTCAACACAAATGGTTCAGTTTCACTGCACTGCCAAATCGAGTGG 60

Subject: 348 TGCTGGACCAACAGAATTCTTCCGCTTTTTTATCTGCGCTTCCAGCTTCTT

Score = 177 (48.9 bits), Expect = 1.5e-58, sum F(5) = 1.5e-58
Identities = 41/48 (85%), Positives = 41/48 (85%), Gaps = 0, Misses = 7

5 Score = 154 (42.6 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 34/38 (89%), Positives = 34/38 (89%), Strand = Minus / Plus

Query: 153 AGAACTTCGTTCTGAAACATGCAGGTCTGGCATCTTG 116

10 subjct: 299 AGAACTTCATCCTGAAGCATAACAGGTCTGGCATCTTG 336

Score = 86 (23.8 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 22/28 (78%), Positives = 22/28 (78%), Strand = Minus / Plus

15 Query: 256 TCCTGCCTTGCAGAATTATTCCATTAT 229

Sbjct: 193 TCCTCCTTTCACAGAATTATTCCAGGAT 220